

## SEQUENCE LISTING

&lt;110&gt; HOFMEISTER, ROBERT ET AL.

&lt;120&gt; Compositions comprising polypeptides

&lt;130&gt; DEBE:066US

&lt;140&gt; UNKNOWN

&lt;141&gt; 2006-05-25

&lt;150&gt; PCT/EP 2004/013445

&lt;151&gt; 2004-11-26

&lt;150&gt; EP 03 027 511.9

&lt;151&gt; 2003-11-28

&lt;160&gt; 6

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 504

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; Construct 1: VL(CD19)-VH(CD19)-VH(CD3)-VL(CD3)

&lt;400&gt; 1

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5					10					15	

Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp
		20					25						30		

Gly	Asp	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Gln	Pro	Pro
	35					40						45			

Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Val	Ser	Gly	Ile	Pro	Pro
	50					55					60				

Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His
65					70					75				80	

Pro	Val	Glu	Lys	Val	Asp	Ala	Ala	Thr	Tyr	His	Cys	Gln	Gln	Ser	Thr
			85						90					95	

Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly
		100					105						110		

Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val
	115					120						125			

Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ser	Ser	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130				135				140							
Lys 145	Ile	Ser	Cys	Lys	Ala 150	Ser	Gly	Tyr	Ala	Phe 155	Ser	Ser	Tyr	Trp	Met 160
Asn	Trp	Val	Lys	Gln 165	Arg	Pro	Gly	Gln	Gly 170	Leu	Glu	Trp	Ile	Gly 175	
Ile	Trp	Pro	Gly 180	Asp	Gly	Asp	Thr	Asn 185	Tyr	Asn	Gly	Lys	Phe 190	Lys	Gly
Lys	Ala	Thr 195	Leu	Thr	Ala	Asp	Glu 200	Ser	Ser	Ser	Thr	Ala 205	Tyr	Met	Gln
Leu	Ser 210	Ser	Leu	Ala	Ser	Glu 215	Asp	Ser	Ala	Val	Tyr 220	Phe	Cys	Ala	Arg
Arg 225	Glu	Thr	Thr	Thr	Val 230	Gly	Arg	Tyr	Tyr	Tyr 235	Ala	Met	Asp	Tyr	Trp 240
Gly	Gln	Gly	Thr	Thr 245	Val	Thr	Val	Ser	Ser 250	Gly	Gly	Gly	Gly	Ser 255	Asp
Ile	Lys	Leu	Gln 260	Gln	Ser	Gly	Ala	Glu 265	Leu	Ala	Arg	Pro	Gly 270	Ala	Ser
Val	Lys 275	Met	Ser	Cys	Lys	Thr	Ser 280	Gly	Tyr	Thr	Phe	Thr 285	Arg	Tyr	Thr
Met 290	His	Trp	Val	Lys	Gln 295	Arg	Pro	Gly	Gln	Gly 300	Leu	Glu	Trp	Ile	Gly
Tyr 305	Ile	Asn	Pro	Ser	Arg 310	Gly	Tyr	Thr	Asn	Tyr 315	Asn	Gln	Lys	Phe	Lys 320
Asp	Lys	Ala	Thr	Leu 325	Thr	Thr	Asp	Lys	Ser 330	Ser	Ser	Thr	Ala	Tyr 335	Met
Gln	Leu	Ser	Ser 340	Leu	Thr	Ser	Glu	Asp 345	Ser	Ala	Val	Tyr	Tyr 350	Cys	Ala
Arg	Tyr 355	Tyr	Asp	Asp	His	Tyr	Cys 360	Leu	Asp	Tyr	Trp	Gly 365	Gln	Gly	Thr
Thr 370	Leu	Thr	Val	Ser	Ser 375	Val	Glu	Gly	Gly	Ser	Gly 380	Gly	Ser	Gly	Gly
Ser 385	Gly	Gly	Ser	Gly 390	Gly	Val	Asp	Asp	Ile	Gln 395	Leu	Thr	Gln	Ser	Pro 400
Ala	Ile	Met	Ser	Ala 405	Ser	Pro	Gly	Glu	Lys 410	Val	Thr	Met	Thr	Cys 415	Arg
Ala	Ser	Ser 420	Ser	Val	Ser	Tyr	Met	Asn 425	Trp	Tyr	Gln	Gln	Lys 430	Ser	Gly
Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly

435                      440                      445  
 Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu  
 450                      455                      460  
 Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln  
 465                      470                      475                      480  
 Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu  
 485                      490                      495  
 Leu Lys His His His His His His  
 500

<210> 2  
 <211> 505  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Construct 2: VH(CD19) -VL(CD19) -VH(CD3) -VL(CD3)

<400> 2

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser  
 1                      5                      10                      15  
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr  
 20                      25                      30  
 Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
 35                      40                      45  
 Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe  
 50                      55                      60  
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr  
 65                      70                      75                      80  
 Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 85                      90                      95  
 Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp  
 100                      105                      110  
 Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly  
 115                      120                      125  
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr  
 130                      135                      140  
 Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile  
 145                      150                      155                      160  
 Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu

				165					170					175			
Asn	Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr		
			180					185					190				
Asp	Ala	Ser	Asn	Leu	Val	Ser	Gly	Ile	Pro	Pro	Arg	Phe	Ser	Gly	Ser		
		195					200					205					
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Lys	Val		
	210					215					220						
Asp	Ala	Ala	Thr	Tyr	His	Cys	Gln	Gln	Ser	Thr	Glu	Asp	Pro	Trp	Thr		
225					230					235					240		
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Ser	Gly	Gly	Gly	Gly	Ser		
				245					250					255			
Asp	Ile	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala		
			260					265					270				
Ser	Val	Lys	Met	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr		
		275					280					285					
Thr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile		
	290					295					300						
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe		
305					310					315					320		
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr		
				325					330					335			
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys		
			340					345					350				
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly		
		355					360					365					
Thr	Thr	Leu	Thr	Val	Ser	Ser	Val	Glu	Gly	Gly	Ser	Gly	Gly	Ser	Gly		
	370					375					380						
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser		
385					390					395					400		
Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys		
			405						410					415			
Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser		
			420					425					430				
Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser		
	435						440					445					
Gly	Val	Pro	Tyr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser		
	450					455					460						
Leu	Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys		

465		470		475		480
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu						
	485			490		495

Glu Leu Lys His His His His His His
500 505

<210> 3  
 <211> 504  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Construct 6: VH(CD3) -VL(CD3) -VH(CD19) -VL(CD19)

<400> 3

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile
130 135 140

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
145 150 155 160

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser
165 170 175

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
180 185 190

Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
195 200 205

Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 210 215 220  
 Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 225 230 235 240  
 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu  
 245 250 255  
 Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly  
 260 265 270  
 Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly  
 275 280 285  
 Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr  
 290 295 300  
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu  
 305 310 315 320  
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp  
 325 330 335  
 Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg  
 340 345 350  
 Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val  
 355 360 365  
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 370 375 380  
 Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu  
 385 390 395 400  
 Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr  
 405 410 415  
 Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro  
 420 425 430  
 Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro  
 435 440 445  
 Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile  
 450 455 460  
 His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser  
 465 470 475 480  
 Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 485 490 495  
 Ser Gly His His His His His His  
 500

<210> 4  
<211> 503  
<212> PRT  
<213> artificial sequence

<220>  
<223> Construct 8: VH(CD3) -VL(CD3) -VL(CD19) -VH(CD19)

<400> 4

Asp	Ile	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala	
1				5					10					15		
Ser	Val	Lys	Met	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	
			20					25					30			
Thr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	
		35					40					45				
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	
	50					55					60					
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	
65					70					75					80	
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	
			100					105					110			
Thr	Thr	Leu	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
		115					120					125				
Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ile	
	130					135					140					
Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	
145					150					155					160	
Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	
				165					170					175		
Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val	Pro	
			180					185					190			
Tyr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	
		195					200					205				
Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	
	210					215					220					
Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	
225					230					235					240	

Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser  
 245 250 255  
 Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser  
 260 265 270  
 Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln  
 275 280 285  
 Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu  
 290 295 300  
 Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 305 310 315 320  
 Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr  
 325 330 335  
 His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr  
 340 345 350  
 Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
 355 360 365  
 Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val  
 370 375 380  
 Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala  
 385 390 395 400  
 Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly  
 405 410 415  
 Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr  
 420 425 430  
 Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser  
 435 440 445  
 Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala  
 450 455 460  
 Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr  
 465 470 475 480  
 Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 485 490 495  
 Gly His His His His His His  
 500

<210> 5  
 <211> 504  
 <212> PRT  
 <213> artificial sequence



<220>

<223> Construct 5: VL(CD3)-VH(CD3)-VH(CD19)-VL(CD19)

<400> 5

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	
1				5					10					15		
Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	
			20					25					30			
Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	
		35					40					45				
Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val	Pro	Tyr	Arg	Phe	Ser	Gly	Ser	
	50					55					60					
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	
65					70					75					80	
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	
				85					90					95		
Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Gly	Gly	Gly	Gly	Ser	Gly	
			100					105					110			
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Lys	Leu	Gln	Gln	Ser	
			115					120					125			
Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	
	130					135						140				
Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp	Val	Lys	Gln	
145					150					155					160	
Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser	Arg	
			165						170					175		
Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	
			180					185					190			
Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	
	195						200					205				
Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Tyr	Asp	Asp	His	
	210					215					220					
Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	
225					230					235					240	
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	
				245					250					255		
Leu	Val	Arg	Pro	Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
			260					265					270			
Tyr	Ala	Phe	Ser	Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	

275					280					285						
Gln	Gly	Leu	Glu	Trp	Ile	Gly	Gln	Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	
290					295					300						
Asn	Tyr	Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Glu	
305					310					315					320	
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	
325					330					335						
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Arg	Glu	Thr	Thr	Thr	Val	Gly	Arg	
340					345					350						
Tyr	Tyr	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	
355					360					365						
Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
370					375					380						
Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	
385					390					395					400	
Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	
405					410					415						
Asp	Gly	Asp	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Gln	Pro	
420					425					430						
Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Val	Ser	Gly	Ile	Pro	
435					440					445						
Pro	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	
450					455					460						
His	Pro	Val	Glu	Lys	Val	Asp	Ala	Ala	Thr	Tyr	His	Cys	Gln	Gln	Ser	
465					470					475					480	
Thr	Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	
485					490					495						
Ser	Gly	His	His	His	His	His	His	His								
500																

<210> 6  
 <211> 503  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Construct 7: VL(CD3)-VH(CD3)-VL(CD19)-VH(CD19)

<400> 6

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly
1				5					10					15	

Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	20	25	30
Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	35	40	45
Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val	Pro	Tyr	Arg	Phe	Ser	Gly	Ser	50	55	60
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	65	70	75
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	85	90	95
Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Gly	Gly	Gly	Gly	Ser	Gly	100	105	110
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Lys	Leu	Gln	Gln	Ser	115	120	125
Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	130	135	140
Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp	Val	Lys	Gln	145	150	155
Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser	Arg	165	170	175
Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	180	185	190
Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	195	200	205
Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Tyr	Asp	Asp	His	210	215	220
Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	225	230	235
Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ser	245	250	255
Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	260	265	270
Gln	Ser	Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	275	280	285
Ile	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	290	295	300
Val	Ser	Gly	Ile	Pro	Pro	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	305	310	315

Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Lys	Val	Asp	Ala	Ala	Thr	Tyr	325	330	335	
His	Cys	Gln	Gln	Ser	Thr	Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	340	345	350	
Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	355	360	365	
Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	370	375	380	
Arg	Pro	Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	385	390	395	400
Phe	Ser	Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	405	410	415	
Leu	Glu	Trp	Ile	Gly	Gln	Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	420	425	430	
Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Glu	Ser	Ser	435	440	445	
Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala	450	455	460	
Val	Tyr	Phe	Cys	Ala	Arg	Arg	Glu	Thr	Thr	Thr	Val	Gly	Arg	Tyr	Tyr	465	470	475	480
Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	485	490	495	
Gly	His	His	His	His	His	His	His									500			